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<!--StartFragment-->RESULT 2
ADC00348
ID    ADC00348 standard; protein; 441 AA.                                Appendix  A
XX
AC    ADC00348;
XX
DT    15-JUN-2007 (revised)
DT    04-DEC-2003 (first entry)
XX
DE    Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 393.
XX
KW    enterohaemorrhagic; anti-bacterial; BOND_PC; hypothetical protein;
KW    hypothetical protein ECs1812 [Escherichia coli O157:H7];
KW    hypothetical protein ECs1812 [Escherichia coli O157:H7 str. Sakai];
KW    unknown protein encoded by cryptic prophage CP-933P;
KW    hypothetical protein [Escherichia coli O157:H7 str. Sakai].
XX
OS    Escherichia coli; O157:H7.
XX
PN    JP2002355074-A.
XX
PD    10-DEC-2002.
XX
PF    24-JAN-2002; 2002JP-00015959.
XX
PR    24-JAN-2001; 2001JP-00112010.
XX
PA    (UYTS-) UNIV TSUKUBA.
XX
DR    WPI; 2003-451640/43.
DR    PC:NCBI; gi13259568.
XX
PT    Enterohemorrhagic Escherichia coli O157:H7-specific nucleic acid molecule
PT    and a polypeptide and its use, a polypeptide, a vector and a host cell.
XX
PS    Claim 3; SEQ ID NO 393; 2067pp; Japanese.
XX
CC    The invention relates to a novel enterohaemorrhagic Escherichia coli
CC    O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
CC    has anti-bacterial activity. The polypeptide can be used in detection
CC    and/or treatment of O157:H7 infection. The nucleotide sequence of the
CC    genome of Enterohaemorrhagic E coli O157:H7 was determined. The present
CC    sequence represents an E. coli O157:H7-specific polypeptide of the
CC    invention.
CC
CC    Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC    information from BOND.
XX
SQ    Sequence 441 AA;

Query Match      84.1%; Score 1943.5; DB 6; Length 441;
Best Local Similarity 81.0%; Pred. No. 5.8e-175;
Matches 359; Conservative 32; Mismatches 37; Indels 15; Gaps 3;

Qy      1 MNIQPNHSGITTONNQHHHAEQVPVSSSIPRSDLPPNCEAGFVHHIPEDIQQHVPECG 60
      ||||| | ||||| || || ||| | : |||: || | :|||: || ||||| ||||| ||||
Db      1 MNIQPTIQSGITSQNN-QHHQTEQIP-STQIPQSELPLGCQAGFVFNIPDDIQHHAPECG 58

Qy      61 ETTALLSLIKDEGLLSGLDKYLAPHLEEGSLGKKALDTFGLFNVTQMALEIPSSVPGISG 120
      ||||| ||||| ||||| ||| ||| ||||| ||| || ||||| ||||| ||||| |||||
Db      59 ETTALLSLIKDKGLLSGLDEYIAPHLEEGSIGKKTLDMFGLFNVTQMALEIPSSVSGISG 118

Qy      121 KYGVQMNIVKPDIHPTTGNFYFLQFLPHDEIGFNFKDPLGPKLNALNTSSSI----- 171
      ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      119 KYGVQLNIVKPDIHPTSGNYFLQIFPLHDEIGFNFKDPLGPKLNALNSNISTTAVSTIA 178

Qy      172 ----SATASTVAPTNDPMPWFGLTAQVVRNHGVLELIVKTENGWKLIVGETPLTPDGPKA 227
  
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[illegible]